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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/715,036

DATE: 05/29/2001

TIME: 13:03:27

Input Set : A:\77281104.app

Output Set: C:\CRF3\05292001\I715036.raw

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3 <110> APPLICANT: DODO, HORTENSE W.  
4 ARNTZEN, CHARLES J.  
5 KONAN, KOFFI N'DA  
6 VIQUEZ, OLGA  
8 <120> TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN  
9 TRANSGENIC PEANUT SEEDS  
11 <130> FILE REFERENCE: 072121/0104  
13 <140> CURRENT APPLICATION NUMBER: 09/715,036  
14 <141> CURRENT FILING DATE: 2000-11-20  
16 <150> PRIOR APPLICATION NUMBER: 60/167,255  
17 <151> PRIOR FILING DATE: 1999-11-19  
19 <160> NUMBER OF SEQ ID NOS: 8  
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24 <211> LENGTH: 1162  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Arachis hypogaea  
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29 <221> NAME/KEY: CDS  
30 <222> LOCATION: (110)..(730)  
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36 Met Ala Lys  
37 1  
39 ctc acc ata cta gta gcc ctc gcc ctt ttc ctc ctc gct gcc cac gca 166  
40 Leu Thr Ile Leu Val Ala Leu Ala Leu Phe Leu Leu Ala Ala His Ala  
41 5 10 15  
43 tct gcg agg cag cag tgg gaa ctc caa gga gac aga aga tgc cag agc 214  
44 Ser Ala Arg Gln Gln Trp Glu Leu Gln Gly Asp Arg Arg Cys Gln Ser  
45 20 25 30 35  
47 cag ctc gag agg gcg aac ctg agg ccc tgc gag caa cat ctc atg cag 262  
48 Gln Leu Glu Arg Ala Asn Leu Arg Pro Cys Glu Gln His Leu Met Gln  
49 40 45 50  
51 aag atc caa cgt gac gag gat tca tat gaa cgg gac ccg tac agc cct 310  
52 Lys Ile Gln Arg Asp Glu Asp Ser Tyr Glu Arg Asp Pro Tyr Ser Pro  
53 55 60 65  
55 agt cag gat ccg tac agc cct agt cca tat gat cgg aga ggc gct gga 358  
56 Ser Gln Asp Pro Tyr Ser Pro Ser Pro Tyr Asp Arg Arg Gly Ala Gly  
57 70 75 80  
59 tcc tct cag cac caa gag agg tgt tgc aat gag ctg aac gag ttt gag 406  
60 Ser Ser Gln His Gln Glu Arg Cys Cys Asn Glu Leu Asn Glu Phe Glu  
61 85 90 95  
63 aac aac caa agg tgc atg tgc gag gca ttg caa cag atc atg gag aac 454  
64 Asn Asn Gln Arg Cys Met Cys Glu Ala Leu Gln Gln Ile Met Glu Asn  
65 100 105 110 115  
67 cag agc gat agg ttg cag ggg agg caa cag gag caa cag ttc aag agg 502

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68 Gln Ser Asp Arg Leu Gln Gly Arg Gln Gln Glu Gln Gln Phe Lys Arg
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72 Glu Leu Arg Asn Leu Pro Gln Gln Cys Gly Leu Arg Ala Pro Gln Arg
73          135          140          145
75 tgc gac ttg gac gtc gaa agt ggc ggc agg cgg ccg cga att ccg ccg 598
76 Cys Asp Leu Asp Val Glu Ser Gly Gly Arg Arg Pro Arg Ile Pro Pro
77          150          155          160
79 ata ctg acg ggc tcc agg agt cgt cgc cac caa tcc cca tat gga aac 646
80 Ile Leu Thr Gly Ser Arg Ser Arg Arg His Gln Ser Pro Tyr Gly Asn
81          165          170          175
83 cgt cga tat tca gcc atg tgc ctt ctt ccg cgt gca gca gat ggc gat 694
84 Arg Arg Tyr Ser Ala Met Cys Leu Leu Pro Arg Ala Ala Asp Gly Asp
85 180          185          190          195
87 ggc tgg ttt cca tca gtt gct gtt gac tgt agc ggc tgatgttgaa 740
88 Gly Trp Phe Pro Ser Val Ala Val Asp Cys Ser Gly
89          200          205
91 ctggaagtcg ccgcgccact ggtgtgggcc ataattcaat tcgcgcgtcc cgcagcgcag 800
93 accgtttttc ctcggaaga cgtacgggt atacatgtct gacaatggca gatcccagcg 860
95 gtcaaaacag gcgcgagtaa ggcggtcggg atagttttct tcgggcccta atccgagcca 920
97 gtttaccgcg tctgctacct gcgccagctg gcagttcaag ccaatccgcg ccggatgcgg 980
99 tgtatcgctc gccacttcaa catcaacggt aatcgccatt tgaccactac catcaatccg 1040
101 gtaggttttc cggctgataa ataaaggttt tcccctgatg ctgccacgcg tgagcggtcg 1100
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110 <212> TYPE: PRT
111 <213> ORGANISM: Arachis hypogaea
113 <400> SEQUENCE: 2
114 Met Ala Lys Leu Thr Ile Leu Val Ala Leu Ala Leu Phe Leu Leu Ala
115 1 5 10 15
117 Ala His Ala Ser Ala Arg Gln Gln Trp Glu Leu Gln Gly Asp Arg Arg
118 20 25 30
120 Cys Gln Ser Gln Leu Glu Arg Ala Asn Leu Arg Pro Cys Glu Gln His
121 35 40 45
123 Leu Met Gln Lys Ile Gln Arg Asp Glu Asp Ser Tyr Glu Arg Asp Pro
124 50 55 60
126 Tyr Ser Pro Ser Gln Asp Pro Tyr Ser Pro Ser Pro Tyr Asp Arg Arg
127 65 70 75 80
129 Gly Ala Gly Ser Ser Gln His Gln Glu Arg Cys Cys Asn Glu Leu Asn
130 85 90 95
132 Glu Phe Glu Asn Asn Gln Arg Cys Met Cys Glu Ala Leu Gln Gln Ile
133 100 105 110
135 Met Glu Asn Gln Ser Asp Arg Leu Gln Gly Arg Gln Gln Glu Gln Gln
136 115 120 125
138 Phe Lys Arg Glu Leu Arg Asn Leu Pro Gln Gln Cys Gly Leu Arg Ala
139 130 135 140
141 Pro Gln Arg Cys Asp Leu Asp Val Glu Ser Gly Gly Arg Arg Pro Arg

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142 145          150          155          160
144 Ile Pro Pro Ile Leu Thr Gly Ser Arg Ser Arg Arg His Gln Ser Pro
145          165          170          175
147 Tyr Gly Asn Arg Arg Tyr Ser Ala Met Cys Leu Leu Pro Arg Ala Ala
148          180          185          190
150 Asp Gly Asp Gly Trp Phe Pro Ser Val Ala Val Asp Cys Ser Gly
151          195          200          205
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159 <400> SEQUENCE: 3
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162 gaggcagcag tgggaactcc aaggagacag aagatgccag agccagctcg agaggcgcaa 180
163 cctgaggccc tgcgagcaac atctcatgca gaagatccaa cgtgacgagg attcatatga 240
164 acgggaccgc tacagcccta gtcaggatcc gtacagccct agtccatag atcggagagg 300
165 cgctggatcc tctcagcacc aagagaggtg ttgcaatgag ctgaacgagt ttgagaacaa 360
166 ccaaaggtgc atgtgcgagg cattgcaaca gatcatggag aaccagagcg ataggttgca 420
167 ggggaggcaa caggagcaac agttcaagag ggagctcagg aacttgccct aacagtgcgg 480
168 ccttagggca ccacagcggt gcgacttgga cgtcgaaagt ggcggcaggc ggccgcgaat 540
169 tccgccgata ctgacggggt ccaggagtcg tcgccacca tccccatag gaaaccgtcg 600
170 atattcagcc atgtgccttc ttccgcgtgc agcagatggc gatggctggt ttccatcagt 660
171 tgctgttgac tgtagcgggt ga                                     682
174 <210> SEQ ID NO: 4
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176 <212> TYPE: DNA
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182 agacctgaca accgcattga atcggagggc ggttacattg agacttgga cccaacaac 180
183 caggagttcg aatgcgccgg cgctgccctc tctcgcttag tctccgccg caacgccctt 240
184 cgtaggcctt tctactccaa tgctccccag gagatcttca tccagcaagg aaggggatac 300
185 tttgggttga tattccctgg ttgtcctagc acatatgaag agcctgcaca acaaggacgc 360
186 cgatatcagt cccaaagacc accaagacgt ttgcaagaag aagaccaag ccaacagcaa 420
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188 ggtgttgctt tctggctgta caacgaccac gacactgatg ttggtgctgt ttctcttact 540
189 gacaccaaca actacgacaa ccagcttgat cagttcccca ggagattcaa tttggctggg 600
190 aaccacgagc aagagttctt aaggtaccag caacaaagca gacaaagcag acgaagaagc 660
191 ttaccatata gccatacag cccgcatagt cggcctagac gagaagagcg tgaatttcgc 720
192 cctcgaggac agcacagccg cagagaacga gcaggacaag aagaagaaga cgaaggtgga 780
193 aacatcttca gcggtttcac gccggagttc ctggaacaag ccttccaggt tgacgacaga 840
194 cagattgtgc aaaatctgtg gggcgagaac gagagtgaag aagagggagc cattgtgacg 900
195 gtgaggggag gcctcagaat cttgagccca gatggaacga gaggtgccga cgaagaagag 960
196 gaatacgaat aagatcaata tgaataccat gaacaggatg gaaggcgtgg caggggaagc 1020
197 agaggcgggg ggaatggtat tgaagagacg atctgcaccg catgtgttaa aaagaacatt 1080
198 ggtggaaaca gatcccctca catctacgat cctcagcgct ggttctactca aaactgccac 1140
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200 aggaatgcat tgtttgtccc tcaactacaac accaacgcac acagcatcat atatgcattg 1260
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202 cttcaagagg gtcacgttct tgtgggtgcca cagaacttcg ccgtggctgg gaagtcccag 1380
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204 gccggtgaaa actccttcat agataacctg ccggaggagg tggttgcaaa ttcatatggc 1500
205 ctcccaaggg agcaggcaag gcagcttaag aacaacaacc cttcaagtt cttcgttcca 1560
206 ccttttcagc agtctccgag ggctgtggct taaaaacgac cagtatcttt tgcaagcgtg 1620
207 ttatccacta acataacttt ttgccacaaa tgaataatat aataataaga agaataatgt 1680
208 agttttaatt tttagtatga ataagaatac aaaggggcat tgatgccttt ttgtttaaga 1740
209 tcggaatgta acatatgtgc aatgagcaga tatggagaaa accttttgcg ggaaaaacat 1800
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216 <213> ORGANISM: Arachis hypogaea
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221 tgccaagtca tcaccttacc agaagaaaac agagaacccc tgcgccaga ggtgcctcca 180
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226 aagagaagaa gactggagac aaccaagaga agattggagg cgaccaagtc atcagcagcc 480
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228 tgtgagggaa gaaacatctc ggaacaacct tttctacttc ccgtcaaggc ggttttagcac 600
229 ccgtacggg aaccaaaccg gtaggatccg ggtcctgcag aggtttgacc aaaggtcaag 660
230 gcagtttcag aatctccaga atcaccgtat tgtgcagatc gaggccaaac ctaacactct 720
231 tgttcttccc aagcacgtg atgtgataa catccttgtt atccagcaag ggcaagccac 780
232 cgtgaccgta gcaaattgca ataacagaaa gagctttaat cttgacgagg gccatgcact 840
233 cagaatccca tccggtttca tttctacatc cttgaaccgc catgacaacc agaacctcag 900
234 agtagctaaa atctccatgc ccgttaacac acccgccag tttgaggatt tcttcccgcc 960
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246 cgaactccat ctgcttggct tcggtatcaa cgctgaaaac aaccacagaa tcttcttgc 1680
247 aggtgataag gacaatgtga tagaccagat agagaagcaa gcgaaggatt tagcattccc 1740
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263 gagctctcat ttccctcagt tcaagcctga ggaaattact gctatcatga acgactttgc 180
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266 gaagacgaat caggcgtaa tcatcggaat ctacgataag ccaatgactc cggggcagtg 360
267 caacatgatt gttgaaaggc tgggtgatta tctcattgat acgggtcttt aagtcctctt 420
268 tgttatttct tggtatctgc ttgcttattt cactggctcc tatacgaggc ttgcgcatcg 480
269 tgtgccaaga gaatgctcga ttgtagtgtg ataataattt ttgatgggta ttcaaaagtc 540
270 atgggatctg cgtctaggga agaagttatg gtgcttgaga agtgaatgat aactatcatc 600
271 tctgtgtgtg tgctttttag cgggtatctg tatacaattt acaagtgggt ttaatgctgt 660
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273 aaaaaaaaaa aaaaaaaaaa aaa 743
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279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
282 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe
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286 ctccaaggag acagaagatg 80
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290 <211> LENGTH: 62
291 <212> TYPE: DNA
292 <213> ORGANISM: Artificial Sequence
294 <220> FEATURE:
295 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe
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